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G174A or S  
Y175N or Q or D or E;  
D176L;  
L177I;  
E180N or M;  
V181I or T;  
N182R or C or E or G or H or I or L or K or M or P or T or W or Y or V;  
G183A;  
S184D or N or E or Q or L or I or T or R or K;  
W212N or A or T;  
A246T;  
D293A or R or N or C or Q or E or G or H or I or L or K or M or S or T or V;  
A302R or N or D or C or Q or E or G or H or I or L or K or F or M or P or S or T or W or Y or V;  
R305A or N or D or C or Q or E or G or H or I or L or F or M or P or S or T or W or Y or V;  
Y306A or R or N or D or C or Q or E or G or H or I or L or K or M or P or S or T or W or V;  
D309L;  
Y312Q or N;  
A393R;  
E408C or R;  
L410R or I; and  
S411R or N or Q or E or I or L or K or F or M or P or T or W or Y or V.

30. The variant of claim 29, wherein said homologous glucoamylase is the *Aspergillus niger* G1 glucoamylase.

32. The variant of claim 29, wherein said variant is a truncated glucoamylase.

34. The variant of claim 33, wherein said truncation is at a C- terminal amino acid.

35. The variant of claim 29, wherein said variant comprises a mutation of S119A in the amino acid sequence shown in SEQ ID NO:2 or in a corresponding position in said homologous glucoamylase.

36. The variant of claim 29, wherein said variant comprises a mutation of A302S in the amino acid sequence shown in SEQ ID NO:2 or in a corresponding position in said homologous glucoamylase.

37. The variant of claim 29, wherein said variant comprises a mutation of S411V in the amino acid sequence shown in SEQ ID NO:2 or in a corresponding position in said homologous glucoamylase.

38. The variant of claim 29, wherein said homologous glucoamylase is at least 70% homologous to SEQ ID NO:2.

39. The variant of claim 29, wherein said homologous glucoamylase is at least 80% homologous to SEQ ID NO:2.

40. The variant of claim 29, wherein said homologous glucoamylase is at least 90% homologous to SEQ ID NO:2.

41. The variant of claim 29, wherein said homologous glucoamylase is at least 95% homologous to SEQ ID NO:2.

42. An isolated variant of a parent glucoamylase comprising a mutation at position N236 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in a homologous glucoamylase having at least 60% homology with the amino acid sequence shown in SEQ ID NO:2.

43. An isolated variant of a parent glucoamylase comprising a mutation at position S364 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in a homologous glucoamylase having at least 60% homology with the amino acid sequence shown in SEQ ID NO:2.

44. The variant of claim 43, wherein said variant comprises a mutation of S364A or R or N or D or C or Q or E or G or H or I or L or K or M or F or P or T or W or Y or V in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

45. An isolated variant of a parent glucoamylase comprising a mutation at one or more of the following positions in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in a homologous glucoamylase having at least 60% homology with the amino acid sequence shown in SEQ ID NO:2:

2, 3, 11, 18, 51, 53, 56, 59, 60, 111, 113, 127, 207, 313, 340, 357, 384, 402, and 456.

46. The variant of claim 45, wherein said variant comprises a mutation at position 2 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

47. The variant of claim 46, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

48. The variant of claim 46, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

49. The variant of claim 46, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

50. The variant of claim 46, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

51. The variant of claim 45, wherein said variant comprises a mutation at position 3 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

52. The variant of claim 51, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

53. The variant of claim 51, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

54. The variant of claim 51, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

55. The variant of claim 51, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

56. The variant of claim 45, wherein said variant comprises a mutation at position 11 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

57. The variant of claim 56, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

58. The variant of claim 56, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

59. The variant of claim 56, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

60. The variant of claim 56, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

61. The variant of claim 45, wherein said variant comprises a mutation at position 18 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

62. The variant of claim 61, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

63. The variant of claim 61, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

64. The variant of claim 61, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

65. The variant of claim 61, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

66. The variant of claim 45, wherein said variant comprises a mutation at position 51 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

67. The variant of claim 66, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

68. The variant of claim 66, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

69. The variant of claim 66, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

70. The variant of claim 66, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

71. The variant of claim 45, wherein said variant comprises a mutation at position 53 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

72. The variant of claim 71, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

73. The variant of claim 71, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

74. The variant of claim 71, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

75. The variant of claim 71, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

76. The variant of claim 45, wherein said variant comprises a mutation at position 56 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

77. The variant of claim 76, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

78. The variant of claim 76, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

79. The variant of claim 76, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

80. The variant of claim 76, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

81. The variant of claim 45, wherein said variant comprises a mutation at position 59 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

82. The variant of claim 81, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

83. The variant of claim 81, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

84. The variant of claim 81, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

85. The variant of claim 81, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

86. The variant of claim 45, wherein said variant comprises a mutation at position 60 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

87. The variant of claim 86, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

88. The variant of claim 86, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

89. The variant of claim 86, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

90. The variant of claim 96, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

91. The variant of claim 45, wherein said variant comprises a mutation at position 111 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

92. The variant of claim 91, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

93. The variant of claim 91, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

94. The variant of claim 91, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

95. The variant of claim 91, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

96. The variant of claim 45, wherein said variant comprises a mutation at position 113 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

97. The variant of claim 96, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

98. The variant of claim 96, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

99. The variant of claim 96, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

100. The variant of claim 96, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

101. The variant of claim 45, wherein said variant comprises a mutation at position 127 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

102. The variant of claim 101, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

103. The variant of claim 101, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

104. The variant of claim 101, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

105. The variant of claim 101, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.



106. The variant of claim 45, wherein said variant comprises a mutation at position 207 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

107. The variant of claim 106, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

108. The variant of claim 106, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

109. The variant of claim 106, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

110. The variant of claim 106, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

111. The variant of claim 45, wherein said variant comprises a mutation at position 313 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

112. The variant of claim 111, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

113. The variant of claim 111, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

114. The variant of claim 111, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

115. The variant of claim 111, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

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116. The variant of claim 45, wherein said variant comprises a mutation at position 340 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

117. The variant of claim 116, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

118. The variant of claim 116, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

119. The variant of claim 116, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

120. The variant of claim 116, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

121. The variant of claim 45, wherein said variant comprises a mutation at position 357 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

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122. The variant of claim 121, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

123. The variant of claim 121, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

124. The variant of claim 121, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

125. The variant of claim 121, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

126. The variant of claim 45, wherein said variant comprises a mutation at position 384 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

127. The variant of claim 126, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

128. The variant of claim 126, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

129. The variant of claim 126, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

130. The variant of claim 126, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

131. The variant of claim 45, wherein said variant comprises a mutation at position 402 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

132. The variant of claim 131, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

133. The variant of claim 131, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

134. The variant of claim 131, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

135. The variant of claim 131, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

136. The variant of claim 45, wherein said variant comprises a mutation at position 456 in the amino acid sequence shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.

137. The variant of claim 136, wherein said homologous glucoamylase has at least 70% homology to SEQ ID NO:2.

138. The variant of claim 136, wherein said homologous glucoamylase has at least 80% homology to SEQ ID NO:2.

B 139. The variant of claim 136, wherein said homologous glucoamylase has at least 90% homology to SEQ ID NO:2.

140. The variant of claim 136, wherein said homologous glucoamylase has at least 95% homology to SEQ ID NO:2.

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